



## SEQUENCE LISTING

<110> YOSHINAGA, STEVEN KIYOSHI  
<120> POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE  
<130> A-579B  
<140> US 09/890,729  
<141> 2001-08-03  
<150> PCT US00/01871  
<151> 2000-01-27  
<150> 09/264,527  
<151> 1999-03-08  
<150> 09/244,448  
<151> 1999-02-03  
<160> 37  
<170> PatentIn version 3.2  
<210> 1  
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<220>  
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<222> (1)..(600)

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1 5 10 15  
  
ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca 96  
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
20 25 30  
  
ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144  
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
35 40 45  
  
cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192  
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
50 55 60  
  
ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240  
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
65 70 75 80  
  
atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288  
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95  
  
aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336  
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
100 105 110  
  
att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr			
115	120	125	
ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta		432	
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu			
130	135	140	
ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata		480	
Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile			
145	150	155	160
cct atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac		528	
Leu Ile Ile Trp Phe Ser Lys Lys Tyr Gly Ser Ser Val His Asp			
165	170	175	
cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag		576	
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys			
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195	200		
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<213> Mus musculus			
<400> 2			
Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg			
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20	25	30	
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val			
35	40	45	
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu			
50	55	60	
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro			
65	70	75	80
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu			
85	90	95	
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser			
100	105	110	
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr			
115	120	125	
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu			

130

135

140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Tyr Gly Ser Ser Val His Asp  
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser  
195 200

<210> 3  
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<212> PRT  
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<400> 3

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg  
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Tyr Gly Ser Ser Val His Asp  
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser  
195 200

<210> 4  
<211> 218  
<212> PRT  
<213> Mus musculus

<400> 4

Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln  
1 5 10 15

Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val  
20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu  
35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val  
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg  
65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val  
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe  
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg  
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr  
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val  
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp  
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met  
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala  
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro  
210 215

<210> 5  
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<213> Artificial sequence

<220>  
<223> Synthetic

<400> 5

Met Arg Leu Leu Val Ser Cys Tyr Leu Val Cys Cys Asn Val Phe Leu  
1 5 10 15

Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu  
20 25 30

Trp Leu Val Phe Leu Leu Ile Trp Pro Arg Ala  
35 40

<210> 6  
<211> 966  
<212> DNA  
<213> Mus musculus

<220>  
<221> CDS  
<222> (1)..(966)

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atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cag cct 48  
Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
1 5 10 15

gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96  
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30

ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144  
Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45

gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac 192  
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60

ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa 240  
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln

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atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser 85 90 95				288
cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser 100 105 110				336
ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val 115 120 125				384
acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr 130 135 140				432
gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg Ala Thr Glu Leu Val Lys Ile Leu Glu Val Val Arg Leu Arg Val 145 150 155 160				480
gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn 165 170 175				528
ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro 180 185 190				576
gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp 195 200 205				624
acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr 210 215 220				672
gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val 225 230 235 240				720
ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile 245 250 255				768
agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu 260 265 270				816
acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu 275 280 285				864
gcg gca gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro 290 295 300				912
cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp 305 310 315 320				960
cac gcc His Ala				966

<210> 7  
<211> 322  
<212> PRT  
<213> Mus musculus

<400> 7

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
1 5 10 15

Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30

Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln  
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

<210> 8  
<211> 322  
<212> PRT  
<213> Mus musculus

<400> 8

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
1 5 10 15

Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30

Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln  
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

<210> 9  
<211> 306  
<212> PRT  
<213> Mus musculus  
  
<400> 9

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe  
1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser  
20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
35 40 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
50 55 60

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
100 105 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp  
130 135 140

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr  
145 150 155 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe  
165 170 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile  
180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp  
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly  
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp  
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly  
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys  
260 265 270

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn  
275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val  
290 295 300

Phe Leu  
305

<210> 10  
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<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic

<400> 10

Met Cys Cys Leu Pro Leu Leu Leu Phe Leu Leu Ser Val Val Leu Cys  
1 5 10 15

His Ser Tyr Trp Gln Val Leu Val Tyr Lys Asn Arg Leu Ser Leu Asp  
20 25 30

Cys Val Val Leu Ala Phe Ser Thr Pro Ile Ser Arg Thr Cys Gly Pro  
35 40 45

Pro Trp Asn Ile Thr Thr Val Asn Val Val Val Phe Arg Ser Thr Gly  
50 55 60

Pro Glu Thr  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(864)

<400> 11  
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Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

cga gct gat act cag gag aag gaa gtc aga gcg atg gta ggc agc gac 96  
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

gtg gag ctc agc tgc gct tgc cct gaa gga agc cgt ttt gat tta aat Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn 35 40 45	144
gat gtt tac gta tat tgg caa acc agt gag tcg aaa acc gtg gtg acc Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr 50 55 60	192
tac cac atc cca cag aac agc tcc ttg gaa aac gtg gac agc cgc tac Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr 65 70 75 80	240
cgg aac cga gcc ctg atg tca ccg gcc ggc atg ctg cgg ggc gac ttc Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe 85 90 95	288
tcc ctg cgc ttg ttc aac gtc acc ccc cag gac gag cag aag ttt cac Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His 100 105 110	336
tgc ctg gtg ttg agc caa tcc ctg gga ttc cag gag gtt ttg agc gtt Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val 115 120 125	384
gag gtt aca ctg cat gtg gca gca aac ttc agc gtg ccc gtc gtc agc Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser 130 135 140	432
gcc ccc cac agc ccc tcc cag gat gag ctc acc ttc acg tgt aca tcc Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser 145 150 155 160	480
ata aac ggc tac ccc agg ccc aac gtg tac tgg atc aat aag acg gac Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp 165 170 175	528
aac agc ctg ctg gac cag gct ctg cag aat gac acc gtc ttc ttg aac Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn 180 185 190	576
atg cgg ggc ttg tat gac gtg gtc agc gtg ctg agg atc gca cgg acc Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr 195 200 205	624
ccc agc gtg aac att ggc tgc tgc ata gag aac gtg ctt ctg cag cag Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln 210 215 220	672
aac ctg act gtc ggc agc cag aca gga aat gac atc gga gag aga gac Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp 225 230 235 240	720
aag atc aca gag aat cca gtc agt acc ggc gag aaa aac gcg gcc acg Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr 245 250 255	768
tgg agc atc ctg gct gtc ctg tgc ctt gtg gtc gtg gcg gtg gcc Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala 260 265 270	816
ata ggc tgg gtg tgc agg gac cga tgc ctc caa cac agc tat gca ggt Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly 275 280 285	864

<210> 12  
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<212> PRT  
<213> Homo sapiens

<400> 12

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser  
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp  
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn  
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr  
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln  
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp  
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr  
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala  
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
275 280 285

<210> 13

<211> 267

<212> PRT

<213> Homo sapiens

<400> 13

Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu Leu Ser Cys  
1 5 10 15

Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr  
20 25 30

Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His Ile Pro Gln  
35 40 45

Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu  
50 55 60

Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe  
65 70 75 80

Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu Val Leu Ser  
85 90 95

Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val Thr Leu His  
100 105 110

Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro His Ser Pro  
115 120 125

Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro  
130 135 140

Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp  
145 150 155 160

Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg Gly Leu Tyr  
165 170 175

Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser Val Asn Ile  
180 185 190

Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu Thr Val Gly  
195 200 205

Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn  
210 215 220

Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala  
225 230 235 240

Val Leu Cys Leu Leu Val Val Ala Val Ala Ile Gly Trp Val Cys  
245 250 255

Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
260 265

<210> 14

<211> 276

<212> PRT

<213> Mus musculus

<400> 14

Glu Thr Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys  
1 5 10 15

Ile Asp Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr  
20 25 30

Trp Gln Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr  
35 40 45

Lys Ser Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His  
50 55 60

Leu Ser Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys  
65 70 75 80

Asn Val Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met  
85 90 95

Asn Thr Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu  
100 105 110

Arg Val Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser

115

120

125

Ser Asn Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly  
130 135 140

Tyr Pro Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu  
145 150 155 160

Ile Asp Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly  
165 170 175

Leu Tyr Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly  
180 185 190

Asp Val Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr  
195 200 205

Ser Ile Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro  
210 215 220

Gln Glu Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala  
225 230 235 240

Val Leu Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr  
245 250 255

Arg Pro His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu  
260 265 270

Thr Asp His Ala  
275

<210> 15  
<211> 125  
<212> PRT  
<213> Artificial sequence  
  
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<223> Synthetic  
  
<400> 15

Glu Glu Val Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr  
1 5 10 15

Val Tyr Trp Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg  
20 25 30

Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys  
35 40 45

Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr  
50 55 60

Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn  
65 70 75 80

Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val  
85 90 95

Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly  
100 105 110

Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly  
115 120 125

<210> 16  
<211> 1294  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(199)

<220>  
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<222> (200)..(1105)

<400> 16  
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cgtccgcggg agcgcagtta gagccatct cccgcgcccc gaggttgctc ctctccgagg 120  
tctccgcgg cccaaatctt ccgcgcggcc aggtctccgc gcccgaggt ctccgcggcc 180  
cgaggtctcc gcccgcacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg 232  
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu  
1 5 10

ctc ttc agc agc ctt cga gct gat act cag gag aag gaa gtc aga gcg 280  
Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala  
15 20 25

atg gta ggc agc gac gtg gag ctc agc tgc gct tgc cct gaa gga agc 328  
Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser  
30 35 40

cgt ttt gat tta aat gat gtt tac gta tat tgg caa acc agt gag tcg 376  
Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser  
45 50 55

aaa acc gtg gtg acc tac cac atc cca cag aac agc tcc ttg gaa aac 424  
Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn  
60 65 70 75

gtg gac agc cgc tac cgg aac cga gcc ctg atg tca ccg gcc ggc atg 472  
Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met

	80	85	90	
ctg cgg ggc gac ttc tcc ctg cgc ttg ttc aac gtc acc ccc cag gac Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp				520
95 100 105				
gag cag aag ttt cac tgc ctg gtg ttg agc caa tcc ctg gga ttc cag Glu Gln Lys Phe His Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln				568
110 115 120				
gag gtt ttg agc gtt gag gtt aca ctg cat gtg gca gca aac ttc agc Glu Val Leu Ser Val Glu Val Thr Leu His Val Ala Ala Asn Phe Ser				616
125 130 135				
gtg ccc gtc gtc agc gcc ccc cac agc ccc tcc cag gat gag ctc acc Val Pro Val Val Ser Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr				664
140 145 150 155				
tcc acg tgt aca tcc ata aac ggc tac ccc agg ccc aac gtg tac tgg Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp				712
160 165 170				
atc aat aag acg gac aac agc ctg ctg gac cag gct ctg cag aat gac Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp				760
175 180 185				
acc gtc ttc ttg aac atg cgg ggc ttg tat gac gtg gtc agc gtg ctg Thr Val Phe Leu Asn Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu				808
190 195 200				
agg atc gca cgg acc ccc agc gtg aac att ggc tgc tgc ata gag aac Arg Ile Ala Arg Thr Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn				856
205 210 215				
gtg ctt ctg cag cag aac ctg act gtc ggc agc cag aca gga aat gac Val Leu Leu Gln Gln Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp				904
220 225 230 235				
atc gga gag aga gac aag atc aca gag aat cca gtc agt acc ggc gag Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu				952
240 245 250				
aaa aac gcg gcc acg tgg agc atc ctg gct gtc ctg tgc ctg ctt gtg Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val				1000
255 260 265				
gtc gtg gcg gtg gcc ata ggc tgg gtg tgc agg gac cga tgc ctc caa Val Val Ala Val Ala Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln				1048
270 275 280				
cac agc tat gca ggt gcc tgg gct gtg agt ccg gag aca gag ctc act His Ser Tyr Ala Gly Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr				1096
285 290 295				
ggc cac gtt tgaccggagc tcaccgccca gagcgtggac agggcttccg Gly His Val				1145
300				
tgagacgccca ccgtgagagg ccaggtggca gcttgagcat ggactcccag actgcagggg				1205
agcacttggg gcagccccca gaaggaccac tgctggatcc cagggagaac ctgctggcgt				1265
tggctgtgat cctggaatga ggcccttcc				1294

<210> 17  
<211> 302  
<212> PRT  
<213> Homo sapiens

<400> 17

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser  
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp  
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn  
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr  
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln  
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp  
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr  
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala  
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val  
290 295 300

<210> 18

<211> 302

<212> PRT

<213> Homo sapiens

<400> 18

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser

145	150	155	160
Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp			
165	170	175	
Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn			
180	185	190	
Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr			
195	200	205	
Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln			
210	215	220	
Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp			
225	230	235	240
Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr			
245	250	255	
Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala			
260	265	270	
Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly			
275	280	285	
Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val			
290	295	300	
<210> 19			
<211> 322			
<212> PRT			
<213> Mus musculus			
<400> 19			
Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro			
1	5	10	15
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly			
20	25	30	
Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr			
35	40	45	
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp			
50	55	60	
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln			
65	70	75	80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

<210> 20  
<211> 143  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic

<400> 20

Met Leu Pro Gly Leu Leu Phe Leu Leu Ser Ser Leu Ala Glu Glu Val  
1 5 10 15

Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp  
20 25 30

Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly  
35 40 45

Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val  
50 55 60

Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser  
65 70 75 80

Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp  
85 90 95

Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg  
100 105 110

Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu  
115 120 125

Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His  
130 135 140

<210> 21  
<211> 1370  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (1)..(165)

<220>  
<221> CDS  
<222> (166)..(762)

<400> 21  
aacaatttca cacagggaaac agctatgacc atgattacgc caagctctaa tacgactcac 60

tatagggaaa gctggtacgc ctgcaggtac cggccggaa ttcccggtc gacccacgct	120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc Met Lys Ser Gly	177
1	
ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly	225
5 10 15 20	
gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly	273
25 30 35	
ggt gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys	321
40 45 50	
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr	369
55 60 65	
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His	417
70 75 80	
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp	465
85 90 95 100	
cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro	513
105 110 115	
cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu	561
120 125 130	
tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala	609
135 140 145	
gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt ttg ctt Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu	657
150 155 160	
aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr	705
165 170 175 180	
atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp	753
185 190 195	
gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc Val Thr Leu	802
cagtttcct caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac	862
ttaactacat acatcttctg ctgggtttt gttcaatctg gaagaatgac tgtatcagtc	922
aatggggatt ttaacagact gccttggac tgccgagtcc tctcaaaaca aacaccctct	982

tgcaaccagc tttggagaaa gcccagctcc ttgtgctca ctgggagtgg aatccctgtc	1042
tccacatctg ctcctagcag tgcattcagcc agtaaaacaa acacattac aagaaaaatg	1102
ttttaaagat gccagggta ctgaatctgc aaagcaaatg agcagccaag gaccagcatc	1162
tgtccgcatt tcactatcat actacctctt ctttctgttag ggatgagaat tcctctttta	1222
atcagtcaag ggagatgctt caaagctgga gctattttat ttctgagatg ttgatgtgaa	1282
ctgtacatta gtacatactc agtactctcc ttcaattgct gaaccccaagt tgaccatttt	1342
accaagactt tagatgctt cttgtgcc	1370

<210> 22

<211> 199

<212> PRT

<213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys			
1	5	10	15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile			
20	25	30	

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val			
35	40	45	

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp			
50	55	60	

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu			
65	70	75	80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu			
85	90	95	

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser			
100	105	110	

Ile Phe Asp Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu			
115	120	125	

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro			
130	135	140	

Ile Gly Cys Ala Ala Phe Val Val Cys Ile Leu Gly Cys Ile Leu			
145	150	155	160

Ile Cys Trp Leu Thr Lys Lys Tyr Ser Ser Ser Val His Asp Pro

165

170

175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser  
180 185 190

Arg Leu Thr Asp Val Thr Leu  
195

<210> 23  
<211> 199  
<212> PRT  
<213> Homo sapiens

<400> 23

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys  
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile  
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val  
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp  
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu  
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser  
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu  
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro  
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu  
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Tyr Ser Ser Ser Val His Asp Pro  
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser  
180 185 190

Arg Leu Thr Asp Val Thr Leu  
195

<210> 24  
<211> 200  
<212> PRT  
<213> Mus musculus

<400> 24

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg  
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Tyr Gly Ser Ser Val His Asp  
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser  
195 200

<210> 25	
<211> 24	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 25	
accatgcggc tgggcagtcc tgga	24
<210> 26	
<211> 23	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 26	
tggtgaccta ccacatcccc cag	23
<210> 27	
<211> 23	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 27	
tcccgatgtca ttccctgtct ggc	23
<210> 28	
<211> 24	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 28	
gctctgtctc cggactcaca gccc	24
<210> 29	
<211> 28	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 29	
gtggcagcaa acttcagcgt gcccgtcg	28
<210> 30	
<211> 28	
<212> DNA	

<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 30	
cccaacgtgt actggatcaa taagacgg	28
<210> 31	
<211> 28	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 31	
gcgtgcttag gatcgacgg acccccag	28
<210> 32	
<211> 21	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 32	
gcctctagaa agagctggga c	21
<210> 33	
<211> 21	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 33	
cggcgtttc catttatgag c	21
<210> 34	
<211> 18	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 34	
gcataatttat gaatccca	18
<210> 35	
<211> 18	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> Synthetic oligonucleotide	

<400> 35  
actatttaggg tcatgcac 18

<210> 36  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif

<400> 36

Phe Asp Pro Pro Pro Phe  
1 5

<210> 37  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif

<400> 37

Met Tyr Pro Pro Pro Tyr  
1 5